

MULTIATTRIBUTE MODEL FOR GWAS USING SUPPORT VECTOR REGRESSION WITH PEARSON UNIVERSAL KERNEL

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This work proposes a new methodology to simultaneously select the most relevant SNPs markers for the characterization of any measurable phenotype described by a continuous variable using support vector regression (SVR) with Pearson Universal kernel (Puk). The advantage of using a phenotype quantified by a continuous variable rather than a binary variable is to capture different levels of such characteristics from different genotypes. The proposed methodology is multiattribute towards considering several markers simultaneously to explain the phenotype. Currently, most GWAS studies quantifies the average impact of each marker on the phenotype through linear regressions between a marker and phenotype (monoattribute), in order to indicate the most significant markers in relation to phenotypic trait in question. However, such methods assume that the effects of each marker on the phenotype are only additives, disregarding the possible occurrence of complex interactions such as dominance and epistasis between markers. The Puk has the property of mimicking the behavior of linear kernels, RBF and polynomial, since their parameters are chosen appropriately. Thus, change is the question of what is the kernel to be used and what their parameters for choosing the best kernel parameters Puk to maximize inductive learning of SVR.

Keywords: Support vector regression. Pearson Universal kernel. Genetic markers. GWAS.

Abstract Book

X-meeting BSB 2013-11-10

Mar Hotel

Recife 3-6 November, 2013



X-MEETING BSB 2013

INTERNATIONAL CONFERENCE OF THE ABC & BRAZILIAN SYMPOSIUM ON BIOINFORMATICS

RECIFE - BRAZIL - 03-06 NOV 2013



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Brazilian Association for Bioinformatics and Computer Biology &
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